CLAIMS:

1. Method of identifying chronic EBV associated diseases optionally present in a sample of an individual suspected of or at risk for carrying an EBV associated disease by determining the gene transcription pattern for one or more gene sequence(s), the expression of said sequence(s) being characteristic for respective EBV associated diseases, by amplifying a target sequence within one or more respective RNA(s) transcribed from said gene sequence(s)

wherein the presence of EBV positive cells is determined by amplifying targets from at least one of the following RNA(s):

- the BKRF1 reading frame spanning nucleotides 107950 - 109872 of EBNA-1, and
- a target within exons 2, 3, 4, 5, 6, 7 and 8 spanning nucleotides 58 - 272, 360 - 458, 540 - 788, 871 - 951, 1026 - 1196, 1280 - 1495 and 1574 - 1682 respectively, of LMP-2,

said method further comprising the steps of establishing whether the individual suffers from a lympho-proliferative disease, epithelial tumour and/or chronic active EBV infection by amplifying one or more target sequence(s) selected from the group consisting of

- a target from the BARF1 reading frame spanning nucleotides 165504 – 166166 to establish whether EBV-positive epithelial tumor cells are present

- a target within the BNLF1 reading frame spanning nucleotides 169474-169207 of LMP-1 to determine whether the individual suffers from a lympho-proliferative disease,

– a target within the BCRF1 reading frame spanning nucleotides 8675 - 10184 of vIL10 and/or the BDLF2 reading frame spanning nucleotides 132389-131130 to establish whether the individual suffers from a chronic active EBV infection.

2. ~~Method~~ The method according to claim 1, wherein it is established whether EBV-positive epithelial tumor cells are present by amplifying a target from at least the BARF1 reading frame spanning nucleotides 165504 -166166.

The method

3. ~~Method~~ according to claim 1, wherein it is established whether the individual suffers from a chronic active EBV infection by amplifying a target from at least

- the BCRF1 reading frame spanning nucleotides 8675 -10184 of vIL10 and/or
- the BDLF2 reading frame spanning nucleotides 132389-131130.

The method

4. ~~Method~~ according to claim 1, wherein it is established whether the individual suffers from a lympho-proliferative disease by amplifying a target within the BNLF1 reading frame spanning nucleotides 169474-169207 of LMP-1.

5. Method according to any of claims 1-4 wherein the pairs of oligonucleotides used in the amplification of the respective RNA(s) are selected from the group consisting of:
a pair of oligonucleotides specific for **EBNA-1** consisting of
1.2, 5'-CTCCCTTTACAACCTAAGGC-3' [SEQ.ID.NO.: 2], and
2.1, 5'-AGAGACAAGGTCCTTAATCGCATCC-3' [SEQ.ID.NO.: 3] provided with a T7 polymerase promoter sequence 5'-aattctaatacgactcactataggg-3

and a pair of oligonucleotides specific for **LMP-1** consisting o
1.1, 5'-ATACCTAAGACAAGTTTGCT-3' [SEQ.ID.NO.: 12] provided with a T7 polymerase promoter sequence 5'-aattctaatacgactcactataggg-3', and
2.1, 5'-CATCGTTATGAGTGACTGGA-3' [SEQ.ID.NO.: 14];
and a pair of oligonucleotides specific for **LMP-2** consisting of
1.2, 5'-AGGTACTCTTGGTGCAGCCC-3' [SEQ.ID.NO.: 18], and
2.1, 5'-AGCATATAGGAACAGTCGTGCC-3' [SEQ.ID.NO.: 19] provided with a T7 polymerase promoter sequence 5'-aattctaatacgactcactataggg-3';
and a pair of oligonucleotides specific for **BARF-1** consisting o
1.2, 5'-GGCTGTCACCGCTTTCTTGG-3' [SEQ.ID.NO.: 23], and
2.1, 5'-AGTGTTGGCACTTCTGTGG-3' [SEQ.ID.NO.: 24] provided with a T7 polymerase promoter sequence 5'-aattctaatacgactcactataggg-3',;
and a pair of oligonucleotides specific for **vIL10 (BCRF1)** consisting of
1.1, 5'-TGGAGCGAAGGTTAGTGGTC-3' [SEQ.ID.NO.: 27], and
2.2, 5'-AGACATGGTCTTTGGCTTCAGGGTC-3' [SEQ.ID.NO.: 30] provided with a T7 polymerase promoter sequence 5'-aattctaatacgactcactataggg-3' for;
and a pair of oligonucleotides specific for **BDLF2** consisting of

1.1, 5'-CTACCTTCCACGACTTCACC-3' [SEQ.ID.NO.: 32] provided with a T7 polymerase promoter sequence 5'-aattctaatacgactcactataggg-3' and
2.1, 5'-AGGCCATGGTGTCATCCATC-3' [SEQ.ID.NO.: 34], or
2.2, 5'-AGAGAGAGAGTAGGTCCGCGG-3' [SEQ.ID.NO.: 35].

6. Method according to any of claims 1-5, wherein the RNA is amplified, using a transcription based amplification technique.

7. ~~Method~~ The method according to claim 6, wherein said amplification technique is NASBA.

8. Oligonucleotide, corresponding to part of a nucleic acid sequence encoding Epstein Barr Virus, said oligonucleotide being 10-35 nucleotides in length and comprising, at least a fragment of 10 nucleotides, of a sequence selected from the group consisting of:

- the BKRF1 reading frame spanning nucleotides 107950 - 109872 of EBNA-1,
- the BNLF1 reading frame spanning nucleotides 169474 - 169207 of LMP-1,
- exons 2, 3, 4, 5, 6, 7 and 8 spanning nucleotides 58 - 272, 360 - 458, 540 - 788, 871 - 951, 1026 - 1196, 1280 - 1495 and 1574 - 1682 respectively, of LMP-2,
- the BCRF1 reading frame spanning nucleotides 8675 -10184 of vIL10,
- the BARF1 reading frame spanning nucleotides 165504 -166166, or
- the BDLF2 reading frame spanning nucleotides 132389-131130.

9. Oligonucleotide according to claim 8, being 10-35 nucleotides in length and comprise, at least a fragment of 10 nucleotides, of a sequence selected from the group consisting of:
1.1, 5'-GCCGGTGTGTTGTTCGTATATGG-3' [SEQ.ID.NO.: 1],
1.2, 5'-CTCCCTTTACAACCTAAGGC-3' [SEQ.ID.NO.: 2],
2.1, 5'-AGAGACAAGGTCCTTAATCGCATCC-3' [SEQ.ID.NO.: 3], or
2.2, 5'-AATACAGACAATGGACTCCC-3' [SEQ.ID.NO.: 4], or its complementary sequence (EBNA-1),
or
1.1, 5'-ATACCTAAGACAAGTTTGCT-3' [SEQ.ID.NO.: 12],
1.2, 5'-ATCAACCAATAGAGTCCACCA-3' [SEQ.ID.NO.: 13],
2.1, 5'-CATCGTTATGAGTGACTGGA-3' [SEQ.ID.NO.: 14], or

2.2, 5'-ACTGATGATCACCCTCCTGCTCA-3' [SEQ.ID.NO.: 15], or its complementary sequence (**LMP-1**),
or
1.1, 5'-TAACTGTGGTTTCCATGACG-3' [SEQ.ID.NO.: 17],
1.2, 5'-AGGTACTCTTGGTGCAGCCC-3' [SEQ.ID.NO.: 18],
2.1, 5'-AGCATATAGGAACAGTCGTGCC-3'[SEQ.ID.NO.: 19], or
2.2, 5'-AGTGGACATGAAGAGCACGAA-3' [SEQ.ID.NO.: 20], or its complementary sequence (**LMP-2**),
or
1.1, 5'-CAGGTTCATCGCTCAGCTCC-3' [SEQ.ID.NO.: 22],
1.2, 5'-GGCTGTCACCGCTTTCTTGG-3' [SEQ.ID.NO.: 23],
2.1, 5'-AGTGTTGGCACTTCTGTGG-3' [SEQ.ID.NO.: 24], or
2.2, 5'-AGCATGGGAGATGTTGGCAGC-3' [SEQ.ID.NO.: 25], or its complementary sequence (**BARF-1**),
or
1.1, 5'-TGGAGCGAAGGTTAGTGGTC-3' [SEQ.ID.NO.: 27],
1.2, 5'-TACCTGGCACCTGAGTGTGGAG-3' [SEQ.ID.NO.: 28],
2.1, 5'-AGAATTGGATCATTTCTGACAGGG-3' [SEQ.ID.NO.: 29], or
2.2, 5'-AGACATGGTCTTTGGCTTCAGGGTC-3' [SEQ.ID.NO.: 30], or its complementary sequence (**vIL10 (BCRF1)**),
or
1.1, 5'-CTACCTTCCACGACTTCACC-3' [SEQ.ID.NO.: 32],
1.2, 5'-AAGTCTTTTATAAGGCTCCGGC-3' [SEQ.ID NO.: 33],
2.1, 5'-AGGCCATGGTGTCATCCATC-3' [SEQ.ID.NO.: 34], or
2.2, 5'-AGAGAGAGAGTAGGTCCGCGG-3' [SEQ.ID.NO.: 35], or its complementary sequence (**BDLF2**).

10. Oligonucleotide according to any of claims 8-9 linked to a promoter sequence.

11. Pair of oligonucleotides, for the amplification of a target sequence within a Epstein Barr virus sequence, for use as a set, comprising:
1.2, 5'-CTCCCTTTACAACCTAAGGC-3' [SEQ.ID.NO.: 2], and
2.1, 5'-AGAGACAAGGTCCTTAATCGCATCC-3' [SEQ.ID.NO.: 3] provided with a T7 polymerase promoter sequence 5'-aattctaatacgactcactataggg-3' (**EBNA-1**);
or
1.1, 5'-ATACCTAAGACAAGTTTGCT-3' [SEQ.ID.NO.: 12] provided with a T7 polymerase promoter sequence 5'-aattctaatacgactcactataggg-3', and

2.1, 5'-CATCGTTATGAGTGACTGGA-3' [SEQ.ID.NO.: 14] (**LMP-1**);
or
1.2, 5'-AGGTACTCTTGGTGCAGCCC-3' [SEQ.ID.NO.: 18], and
2.1, 5'-AGCATATAGGAACAGTCGTGCC-3' [SEQ.ID.NO.: 19] provided with a T7 polymerase promoter sequence 5'-aattctaatacgactcactataggg-3' (**LMP-2**);
or
1.2, 5'-GGCTGTCACCGCTTTCTTGG-3' [SEQ.ID.NO.: 23], and
2.1, 5'-AGTGTTGGCACTTCTGTGG-3' [SEQ.ID.NO.: 24] provided with a T7 polymerase promoter sequence 5'-aattctaatacgactcactataggg-3' (**BARF-1**);
or
1.1, 5'-TGGAGCGAAGGTTAGTGGTC-3' [SEQ.ID.NO.: 27], and
2.2, 5'-AGACATGGTCTTTGGCTTCAGGGTC-3' [SEQ.ID.NO.: 30] provided with a T7 polymerase promoter sequence 5'-aattctaatacgactcactataggg-3' (**vIL10 (BCRF1)**);
or
1.1, 5'-CTACCTTCCACGACTTCACC-3' [SEQ.ID.NO.: 32] provided with a T7 polymerase promoter sequence 5'-aattctaatacgactcactataggg-3' and
2.1, 5'-AGGCCATGGTGTCATCCATC-3' [SEQ.ID.NO.: 34], or
2.2, 5'-AGAGAGAGAGTAGGTCCGCGG-3' [SEQ.ID.NO.: 35] (**BDLF2**).

12. Oligonucleotide according to claim 8 being 10-35 nucleotides in length and comprise, at least a fragment of 10 nucleotides, of a sequence selected from the group consisting of:
5'-CGTCTCCCCTTTGGAATGGCCCCTGGACCC-3' [SEQ.ID.NO.: 5] (**EBNA-1**),
5'-GGACAGGCATTGTTCCTTGG-3' [SEQ.ID.NO.: 16] (**LMP-1**),
5'-AGCTCTGGCACTGCTAGCGTCACTGATTTT-3' [SEQ.ID.NO.: 21] (**LMP-2**),
5'-CTGGTTTAAACTGGGCCCAGGAGAGGAGCA-3' [SEQ.ID.NO.: 26] (**BARF-1**),
5'-CAGACCAATGTGACAATTTTCCCCAAATGT-3' [SEQ.ID.NO.: 31] (**vIL10 (BCRF1)**), or
5'-CCAATGGGGGAGGAGAGACCAAGACCAATA-3' [SEQ.ID.NO.: 36] (**BDLF2**),
provided with a detectable label.

13 Test kit for performing the method or claim 1 comprising:
-one or more oligonucleotides according to any of claims 8-9,

-an oligonucleotide comprising a nucleic acid sequence substantially complementary to at least part of the amplified nucleic acid sequence, provided with a detectable label
-suitable amplification reagents.

14. Test kit according to claim 13, wherein said oligonucleotide that is provided with label is an oligonucleotide according to claim 13.

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